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Sequence Listing was accepted.

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Reviewer: Anne Corrigan

Timestamp: [year=2008; month=9; day=23; hr=12; min=55; sec=41; ms=731;]

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Application No: 10585149 Version No: 2.0

Input Set:**Output Set:**

Started: 2008-08-25 13:32:03.562
Finished: 2008-08-25 13:32:06.481
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 919 ms
Total Warnings: 36
Total Errors: 0
No. of SeqIDs Defined: 56
Actual SeqID Count: 56

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 402	Undefined organism found in <213> in SEQ ID (20)
W 402	Undefined organism found in <213> in SEQ ID (21)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
W 213	Artificial or Unknown found in <213> in SEQ ID (23)
W 213	Artificial or Unknown found in <213> in SEQ ID (24)
W 213	Artificial or Unknown found in <213> in SEQ ID (25)
W 213	Artificial or Unknown found in <213> in SEQ ID (26)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)

Input Set:

Output Set:

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Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (29)
W 213	Artificial or Unknown found in <213> in SEQ ID (30) This error has occurred more than 20 times, will not be displayed

SEQUENCE LISTING

<110> BEBBINGTON, CHRISTOPHER ROBERT
YU, BO

<120> TRANSACTIVATION SYSTEM FOR MAMMALIAN CELLS

<130> 73678-026

<140> 10585149

<141> 2008-08-25

<150> PCT/US2004/043830

<151> 2004-12-30

<150> 60/533,917

<151> 2003-12-13

<160> 56

<170> PatentIn version 3.5

<210> 1

<211> 236

<212> PRT

<213> Cricetulus longicaudatus

<400> 1

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Gly	Asp	Val	Asp	Ala	Ala	Pro	Leu	Gly	Ala	Ala	Pro	Thr	Pro	Gly	Ile
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Phe	Ser	Phe	Gln	Pro	Glu	Ser	Asn	Pro	Thr	Pro	Ala	Val	His	Arg	Asp
50						55					60				

Met	Ala	Ala	Arg	Thr	Ser	Pro	Leu	Arg	Pro	Ile	Val	Ala	Thr	Thr	Gly
65					70					75					80

Pro	Thr	Leu	Ser	Pro	Val	Pro	Pro	Val	Val	His	Leu	Thr	Leu	Arg	Arg
				85					90					95	

Ala	Gly	Asp	Asp	Phe	Ser	Arg	Arg	Tyr	Arg	Arg	Asp	Phe	Ala	Glu	Met
				100					105					110	

Ser Ser Gln Leu His Leu Thr Pro Phe Thr Ala Arg Gly Arg Phe Ala
115 120 125

Thr Val Val Glu Glu Leu Phe Arg Asp Gly Val Asn Trp Gly Arg Ile
130 135 140

Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu Ser Val Asn
145 150 155 160

Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp Met Thr Glu
165 170 175

Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn Gly Gly Trp
180 185 190

Asp Ala Phe Val Glu Leu Tyr Gly Pro Ser Val Arg Pro Leu Phe Asp
195 200 205

Phe Ser Trp Leu Ser Leu Lys Thr Leu Leu Ser Leu Ala Leu Val Gly
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Ala Cys Ile Thr Leu Gly Thr Tyr Leu Gly His Lys
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<210> 2

<211> 195

<212> PRT

<213> Cricetulus longicaudatus

<400> 2

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20 25 30

Gly Asp Val Asp Ala Ala Ala Ala Ala Ala Ser Pro Val Pro Pro Val
35 40 45

Val His Leu Thr Leu Arg Arg Ala Gly Asp Asp Phe Ser Arg Arg Tyr
50 55 60

Arg Arg Asp Phe Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro Phe
65 70 75 80

Thr Ala Arg Gly Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg Asp
85 90 95

Gly Val Asn Trp Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val
100 105 110

Met Cys Val Glu Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn
115 120 125

Ile Ala Leu Trp Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp
130 135 140

Ile Gln Asp Asn Gly Gly Trp Asp Ala Phe Val Glu Leu Tyr Gly Pro
145 150 155 160

Ser Val Arg Pro Leu Phe Asp Phe Ser Trp Leu Ser Leu Lys Thr Leu
165 170 175

Leu Ser Leu Ala Leu Val Gly Ala Cys Ile Thr Leu Gly Thr Tyr Leu
180 185 190

Gly His Lys
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<210> 3

<211> 588

<212> DNA

<213> *Cricetulus longicaudatus*

<400> 3

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gccgcgagcc ccgtgccacc tgtggtccac ctgaccctcc gccgggctgg ggatgacttc	180
tcccgtcgct accgtcgca ctccgaggag atgtccagtc agctgcacct gacgccttc	240
accgcgaggg gacgctttgc tacgggtggtg gaggaactct tcagggatgg ggtgaactgg	300
gggaggattg tggccttctt tgagttcggg ggggtcatgt gtgtggagag cgtcaacagg	360
gagatgtcac ccctggtgga caacatcgcc ctgtggatga ccgagtacct gaaccggcat	420
ctgcacacct ggatccagga taacggaggc tgggacgcat ttgtggaact gtacggcccc	480
agtgtgaggc ctctgtttga tttctcttgg ctgtctctga agaccctgct cagcctggcc	540

ctggtcgggg cctgcatcac tctgggtacc tacctgggcc acaagtga

588

<210> 4

<211> 289

<212> PRT

<213> Human adenovirus type 5

<400> 4

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1 5 10 15

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20 25 30

Pro Pro Pro Ser His Phe Glu Pro Pro Thr Leu His Glu Leu His Asp
35 40 45

Leu Asp Val Thr Ala Pro Glu Asp Pro Asn Glu Glu Ala Val Ser Gln
50 55 60

Ile Phe Pro Asp Ser Val Met Leu Ala Val Gln Glu Gly Ile Asp Leu
65 70 75 80

Leu Thr Phe Pro Pro Ala Pro Gly Ser Pro Glu Pro Pro His Leu Ser
85 90 95

Arg Gln Pro Glu Gln Pro Glu Gln Arg Ala Leu Gly Pro Val Ser Met
100 105 110

Pro Asn Leu Val Pro Glu Val Ile Asp Leu Thr Gly His Glu Ala Gly
115 120 125

Phe Pro Pro Ser Asp Asp Glu Asp Glu Glu Gly Glu Glu Phe Val Leu
130 135 140

Asp Tyr Val Glu His Pro Gly His Gly Cys Arg Ser Cys His Tyr His
145 150 155 160

Arg Arg Asn Thr Gly Asp Pro Asp Ile Met Cys Ser Leu Cys Tyr Met
165 170 175

Arg Thr Cys Gly Met Phe Val Tyr Ser Pro Val Ser Glu Pro Glu Pro
180 185 190

Glu Pro Glu Pro Glu Pro Glu Pro Ala Arg Pro Thr Arg Arg Pro Lys
 195 200 205

Met Ala Pro Ala Ile Leu Arg Arg Pro Thr Ser Pro Val Ser Arg Glu
 210 215 220

Cys Asn Ser Ser Thr Asp Ser Cys Asp Ser Gly Pro Ser Asn Thr Pro
 225 230 235 240

Pro Glu Ile His Pro Val Val Pro Leu Cys Pro Ile Lys Pro Val Ala
 245 250 255

Val Arg Val Gly Gly Arg Arg Gln Ala Val Glu Cys Ile Glu Asp Leu
 260 265 270

Leu Asn Glu Pro Gly Gln Pro Leu Asp Leu Ser Cys Lys Arg Pro Arg
 275 280 285

Pro

<210> 5

<211> 986

<212> DNA

<213> Human adenovirus type 5

<400> 5

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cctacccttc acgaactgca tgatttagac gtgacggccc ccgaagatcc caacgaggag	180
gcggtttcgc agatttttcc cgactctgta atgttgccg tgcaggaagg gattgactta	240
ctcacttttc cgccggcgcc cggttctccg gagccgcctc acctttcccg gcagcccgag	300
cagccggagc agagagcctt gggtcgggtt tctatgcaa accttgtagc ggaggtgatc	360
gatcttaccg gccacgaggc tggctttcca ccagtgacg acgaggatga agagggtgag	420
gagtttgtgt tagattatgt ggagcaccac gggcacgggt gcaggtcttg tcattatcac	480
cggaggaata cgggggaccc agatattatg tgttcgcttt gctatatgag gacctgtggc	540
atgtttgtct acagtaagtg aaaattatgg gcagtgggtg atagagtggg gggtttggtg	600
tggtaat ttttttaatt ttacagttt tgtggtttaa agaattttgt attgtgattt	660
ttttaaaagg tcctgtgtct gaacctgagc ctgagcccg gccagaaccg gagcctgcaa	720

gacctaccg cegtcctaaa atggcgctg ctatcctgag acgcccgaca tcacctgtgt	780
ctagagaatg caatagtagt acggatagct gtgactccg tccttctaac acacctcctg	840
agatacacc ggtgggtccg ctgtgcccc ttaaaccagt tgccgtgaga gttggtgggc	900
gtcgccaggc tgtggaatgt atcgaggact tgcttaacga gcctgggcaa cctttggact	960
tgagctgtaa acgcccagg ccataa	986

<210> 6
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 6	
cccgaattcg ccgccacat gagacatatt atctgccac	39

<210> 7
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 7	
cccgtcgacc ttatggcctg gggcgttt	28

<210> 8
 <211> 39
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 primer

<400> 8	
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<210> 9
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic primer

<400> 9
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<210> 10
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 10
ggaggtgatc gatcttaccg gccac 25

<210> 11
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 11
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<210> 12
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 12
cgtcacgtct aaatcatgca gttcgtgaag ggtagg 36

<210> 13
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic primer

<400> 13
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<210> 14
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 14
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<210> 15
<211> 558
<212> DNA
<213> Human adenovirus type 5

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caggcaaagt tagtctgcag aattaaggag gattacaagt gggaatttga agagcttttg 180
aaatcctgtg gtgagctgtt tgattctttg aatctgggtc accaggcgct tttccaagag 240
aaggatcatca agactttgga tttttccaca ccggggcgcg ctgcggctgc tgttgctttt 300
ttgagtttta taaaggataa atggagcgaa gaaacccatc tgagcggggg gtacctgctg 360
gattttctgg ccatgcatct gtggagagcg gttgtgagac acaagaatcg cctgctactg 420
ttgtcttccg tccgcccggc gataataccg acggaggagc agcagcagca gcaggaggaa 480
gccaggcggc ggcggcagga gcagagccca tggaaccgga gagccggcct ggaccctcgg 540
gaatgaatgt tggtcgac 558

<210> 16
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic
primer

<400> 16
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<210> 17
<211> 32

<212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic primer

<400> 17
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<210> 18
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 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (16)..(2799)

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gcc gcc gct gcc gcc gcg gaa ccc ccg gca ccg ccg ccg ccg ccc cct 99
 Ala Ala Ala Ala Ala Ala Glu Pro Pro Ala Pro Pro Pro Pro Pro Pro
 15 20 25

cct gag gag gac cca gag cag gac agc ggc ccg gag gac ctg cct ctc 147
 Pro Glu Glu Asp Pro Glu Gln Asp Ser Gly Pro Glu Asp Leu Pro Leu
 30 35 40

gtc agg ctt gag ttt gaa gaa aca gaa gaa cct gat ttt act gca tta 195
 Val Arg Leu Glu Phe Glu Glu Thr Glu Glu Pro Asp Phe Thr Ala Leu
 45 50 55 60

tgt cag aaa tta aag ata cca gat cat gtc aga gag aga gct tgg tta 243
 Cys Gln Lys Leu Lys Ile Pro Asp His Val Arg Glu Arg Ala Trp Leu
 65 70 75

act tgg gag aaa gtt tca tct gtg gat gga gta ttg gga ggt tat att 291
 Thr Trp Glu Lys Val Ser Ser Val Asp Gly Val Leu Gly Gly Tyr Ile
 80 85 90

caa aag aaa aag gaa ctg tgg gga atc tgt atc ttt att gca cga gtt 339
 Gln Lys Lys Lys Glu Leu Trp Gly Ile Cys Ile Phe Ile Ala Arg Val
 95 100 105

gac cta gat gag atg tcg ttc act tta ctg agc tac aga aaa aca tac 387
 Asp Leu Asp Glu Met Ser Phe Thr Leu Leu Ser Tyr Arg Lys Thr Tyr
 110 115 120

gaa atc agt gtc cat aaa ttc ttt aac tta cta aaa gaa att gat acc 435
 Glu Ile Ser Val His Lys Phe Phe Asn Leu Leu Lys Glu Ile Asp Thr
 125 130 135 140

agt acc aaa gtt gat aat gct atg tca aga ctg ttg aag aag tat gat	483
Ser Thr Lys Val Asp Asn Ala Met Ser Arg Leu Leu Lys Lys Tyr Asp	
145 150 155	
gta ttg ttt gca ctc ttc agc aaa ttg gaa agg aca tgt gaa ctt ata	531
Val Leu Phe Ala Leu Phe Ser Lys Leu Glu Arg Thr Cys Glu Leu Ile	
160 165 170	
tat ttg aca caa ccc agc agt tcg ata tct act gaa ata aat tct gca	579
Tyr Leu Thr Gln Pro Ser Ser Ser Ile Ser Thr Glu Ile Asn Ser Ala	
175 180 185	
ttg gtg cta aaa gtt tct tgg atc aca ttt tta tta gct aaa ggg gaa	627
Leu Val Leu Lys Val Ser Trp Ile Thr Phe Leu Leu Ala Lys Gly Glu	
190 195 200	
gta tta caa atg gaa gat gat ctg gtg att tca ttt cag tta atg cta	675
Val Leu Gln Met Glu Asp Asp Leu Val Ile Ser Phe Gln Leu Met Leu	
205 210 215 220	
tgt gtc ctt gac tat ttt att aaa ctc tca cct ccc atg ttg ctc aaa	723
Cys Val Leu Asp Tyr Phe Ile Lys Leu Ser Pro Pro Met Leu Leu Lys	
225 230 235	
gaa cca tat aaa aca gct gtt ata ccc att aat ggt tca cct cga aca	771
Glu Pro Tyr Lys Thr Ala Val Ile Pro Ile Asn Gly Ser Pro Arg Thr	
240 245 250	
ccc agg cga ggt cag aac agg agt gca cgg ata gca aaa caa cta gaa	819
Pro Arg Arg Gly Gln Asn Arg Ser Ala Arg Ile Ala Lys Gln Leu Glu	
255 260 265	
aat gat aca aga att att gaa gtt ctc tgt aaa gaa cat gaa tgt aat	867
Asn Asp Thr Arg Ile Ile Glu Val Leu Cys Lys Glu His Glu Cys Asn	
270 275 280	
ata gat gag gtg aaa aat gtt tat ttc aaa aat ttt ata cct ttt atg	915
Ile Asp Glu Val Lys Asn Val Tyr Phe Lys Asn Phe Ile Pro Phe Met	
285 290 295 300	
aat tct ctt gga ctt gta aca tct aat gga ctt cca gag gtt gaa aat	963
Asn Ser Leu Gly Leu Val Thr Ser Asn Gly Leu Pro Glu Val Glu Asn	
305 310 315	
ctt tct aaa cga tac gaa gaa att tat ctt aaa aat aaa gat cta gat	1011
Leu Ser Lys Arg Tyr Glu Glu Ile Tyr Leu Lys Asn Lys Asp Leu Asp	
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cga aga tta ttt ttg gat cat gat aaa act ctt cag act gat tct ata	1059
Arg Arg Leu Phe Leu Asp His Asp Lys Thr Leu Gln Thr Asp Ser Ile	
335 340 345	
gac agt ttt gaa aca cag aga aca cca cga aaa agt aac ctt gat gaa	1107
Asp Ser Phe Glu Thr Gln Arg Thr Pro Arg Lys Ser Asn Leu Asp Glu	
350 355 360	

gag gtg aat ata att cct cca cac act cca gtt agg act gtt atg aac 1155
Glu Val Asn Ile Ile Pro Pro His Thr Pro Val Arg Thr Val Met Asn
365 370 375 380

act atc caa caa tta atg atg att tta aat tct gca agt gat caa c